

HUMAN xiap

| SEQ ID NO:3 | M T F N S F E G S - |
|-------------|--|
| 1 | gaaaagggtggacaaggtaattcaagagaatggactttaaacagtttgaaggatct |
| 61 | aaaacttgcgttacccgtcggcataataaggaaagaatttgttagaaaggatttaaataga |
| a | K T C V P A D I N K E E F V E E F N R - |
| 121 | ttaaaaaacttttgcataatttccaaggtagttggtagtcctgtttcaggcatcaacactggcacacgaa |
| a | L K T F A N F P S G S P V S A S T L A R - |
| 181 | gcagggtttatactggtaaggaggataccgtggcggttgcttagttgtcatgcaggct |
| a | A G F L Y T G E G D T V R C F S C H A A - |
| 241 | gttagatagatggcaatatggagactcagcaggatggaaaggacacaggaaagtatcccccaat |
| a | V D R W Q Y G D S A V G R H R K V S P N - |
| 301 | tgcaggattataacaggcttttatcttggaaaatagtgccacgcgtctacaattctgg |
| a | C R F I N G F Y L E N S A T Q S T N S G - |

Fig. 1A

HUMAN xiop

atccagaatggtcagttacaaaacttgtaaaactatctggaaaggcaggatcatttgcctta 420
361 -----+-----+-----+-----+-----+-----+
a I Q N G Q Y K V E N Y L G S R D H F A L -
gacaggccatctgagacacatggcagactatctttgagaactggcagggttagatata 480
421 -----+-----+-----+-----+-----+-----+
a D R P S E T H A D Y L R T G Q V V D I -
tcagacaccatatacccgaggaaccctgccatgtttagaaagaagcttagattaaagtcc 540
481 -----+-----+-----+-----+-----+-----+
a S D T I Y P R N P A M Y C E E A R L K S -
tttcagaactggcccagactatgttcacctaaccccaagaaggatgttagcaaggctggactc 600
541 -----+-----+-----+-----+-----+-----+
a F Q N W P D Y A H L T P R E L A S A G L -
tactacacaggatttgtgaccaaggcagtgcattttgttgtggaaaactgaaaaat 660
601 -----+-----+-----+-----+-----+-----+
a Y Y T G I G D Q V Q C F C C G G K L K N -
tgggaaccttgtgatcggtgcctggtcagaacacacaggcgcacactttccataattgtcttt 720
661 -----+-----+-----+-----+-----+-----+
a W E P C D R A W S E H R R F P N C F F -

Fig. 1B

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3/61

Fig. 1C

HUMAN xiap

4161

Fig. 1D

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Fig. 1E

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attcatagtatactgatttaattctaagtgtaaatttttttat
1801 - - - + - - - + - - - + - - - + - - - + 1860
a
-
tctttcaaggataggcttaacaaatggaggcttttgtatataaaatgtggaggatttaggtta
1861 - - - + - - - + - - - + - - - + - - - + - - - + 1920
a
-
atctcccaatcacataatttgttttgtgtaaaaaggaaataaaatttgtccatgctggtg
1921 - - - + - - - + - - - + - - - + - - - + - - - + 1980
a
-
gaaagatagagatgttttagaggttggttgtgttttaggatttgtccattttct
1981 - - - + - - - + - - - + - - - + - - - + - - - + 2040
a
-
tgtaaagnnataaacacgnacntgtgcggaaatatnttgtaaagtgtatttgccatttttg
2041 - - - + - - - + - - - + - - - + - - - + - - - + 2100
a
-
aaaggatatttaatgtataactatcgaggccaaatgtactgacatggaaaggatgtca
2101 - - - + - - - + - - - + - - - + - - - + - - - + 2160
a
-

HUMAN xiap

Fig. 1G

HUMAN hiap-1

SEQ ID NO:5 1 TCCTTGAGATGTATCAGTATTAGGATTCATGCCATTAAATGCATAGA 60
 C -
 -
 AATGGAAATAATGGAATTTCATTGGCTTTCAAGCCTAGTATTAAACTGATAAAA 61 120
 C -
 -
 GCAAAGCCATGCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCCATTTC 121 180
 C -
 -
 ATTTCATTATGAAACATAGTAGAAAACAGGCATATTCTTATCAAATTGTGAAAAGGCCA 181 240
 C -
 M N I V E N S I F L S N L M K S A N -
 ACACGTTGAACTGAAATAACGACTTGTATGTGAAACTGTACCGAACATGTCTACGTATTCCA 241 300
 C -
 T F E L K Y D L S C E L Y R M S T Y S T -
 CTTTCCTGCTGGGGTTCCCTGTCAGAAAGGAGTCCTGCTGGTTCTATTACA 301 360
 C -
 F P A G V P V S E R S L A R A G F Y Y T -
 8/61

Fig. 2A

HUMAN hiap-1

Fig. 2B

HUMAN hiap-1

| | |
|---|------|
| CATGGCCATTGACTTTCTGTGCCAACAGATCTGGCACGGCTTACTACATAG | 780 |
| C W P L T F L S P T D L A R A G F Y Y I G - | |
| GACCTGGAGACAGAGTGGCTTGCTTGCCTGTGGTGGAAATGAGCAATTGGAAACCGA | 781 |
| C P G D R V A C F A C G G K L S N W E P K - | |
| AGGATAATGCTATGTCAGAACACCTGAGACATTTCCTCCAAATGCCATTAGAAAATC | 841 |
| C D N A M S E H L R H F P K C P F I E N Q - | |
| AGCTTCAAGACACTTCAGATAACACAGTTCTAATCTGAGCATGCAGACACATGCC | 901 |
| C L Q D T S R Y T V S N L S M Q T H A A R - | |
| GCCTTAAACATTCCTTAACCTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGC | 961 |
| C F K T F F N W P S S V L V N P E Q L A S - | |
| GTGGGGTTTATTATGGTAAACAGTGAATGTCAAATGCTTGGTGTGTC | 1021 |
| C A G F Y Y V G N S D D V K C F C C D G G - | |

Fig. 2C

HUMAN hiap-1

1081 GACTCAGGTGGGAATCTGGAGATGCCATGGGTTCAACATGCCAAGTGGTTCCAA 1140
C L R C W E S G D D P W V Q H A K W F P R -
GGTGTGAGTGTACTTGATAAGAATTAAAGGACACGGAGTTCATCCGTCAAGTICAAGGCCAGTT 1141
C C E Y L I R I K G Q E F F I R Q V Q A S Y -
ACCCCTCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAAATGCAG 1201
C P H L L E Q L L S T S D S P G D E N A E -
AGTCATCAATTATCCATTGGAACCTGGAGAACGACATTCAAAGATGCCAATCATGATGA 1261
C S S I I H L E P G E D H S E D A I M M N -
ATACTCCTGTGATTAAATGCTGCCGTGGAATGGGCTTTAGTAGAAGCCTGGTAAACAGA 1321
C T P V I N A A V E M G F S R S L V K Q T -
CAGTTCAGAGAAATTCTAGCAACTGGAGAGAATTATAAGACTAGTCAATGATCTTGTGT 1381
C V Q R K I L A T G E N Y R L V N D L V L -

11/61

Fig. 2D

HUMAN hiap-1

| | | |
|------|---|------|
| 1441 | TAGACTTACTCAAATGCCAGAAGATGAAATAAGGGAAAGAGGAGAGAAAGAGCAACTGAGG | 1500 |
| C | D L L N A E D E I R E E E R E R A T E E - | |
| 1501 | AAAAGAATCAAATGATTATTAAATCCGGAAAGAAATAGAAATGGCACTTTTCACATT | 1560 |
| C | K E S N D L L I R K N R M A L F Q H L - | |
| 1561 | TGACTTGTGTAATTCCAATCCTGGATAGCTACTAACCTGCGGAATTAAATGAACAAAG | 1620 |
| C | T C V I P I L D S L L T A G I I N E Q E - | |
| 1621 | AACATGATGTTATTAAACAGAAGACACAGACGTCTTACAAGCAAGAGAACTGATTGATA | 1680 |
| C | H D V I K Q K T Q T S L Q A R E L I D T - | |
| 1681 | CGATTITAGTAAAGGAAATAATGGAGCCACTGTATTCAAGAAACTCTCTGCAGAAAGCTG | 1740 |
| C | I L V K G N I A A T V F R N S L Q E A E - | |
| 1741 | AAGCTGTGTTATATGAGCATTATTGTGCAACAGGCACATAATAATATTCCACAGAAG | 1800 |
| C | A V L Y E H L F V Q Q D I K Y I P T E D - | |

Fig. 2E

HUMAN hiap-1

ATGTTCACTTACCAAGTGGAAAGAACATTGGAGACTACCAGAAGAACATGTA
1801 - +-----+-----+-----+-----+-----+-----+-----+ 1860

c V S D L P V E Q L R R L P E E R T C K -

AAGTGTGTATGGACAAAGAACATAGTGTCCATAGTTATTCCCTTGTGGTCATCTAGTAT
1861 - +-----+-----+-----+-----+-----+-----+-----+ 1920

c V C M D K E V S I V F I P C G H L V V C -

GCAAAGATTGTGCTCCTTCTTAAGAACATTGGAGGTACAATCAAGGGTA
1921 - +-----+-----+-----+-----+-----+-----+-----+ 1980

c K D C A P S L R K C P I C R S T I K G T -

CAGTTGTACATTCTTCTATGAAGAACAAACATGGCTAAACTTGAATAAT
1981 - +-----+-----+-----+-----+-----+-----+-----+ 2040

c V R T F L S *

TTATTAAATGTATTAACTTAACTTTATCCTAATTGTTGCCTTAAATTTTATT
2041 - +-----+-----+-----+-----+-----+-----+-----+ 2100

c TATTACAACCTCAAAACATTGTTGTGTAACATATTATATGTAATCTAACCCATA
2101 - +-----+-----+-----+-----+-----+-----+-----+ 2160

Fig. 2F

HUMAN hiap-1

2161 TGAACATATTTAGAAACTAAGAGAATGATAAGCTTTGTCTTATGAAACGAAAA 2220
C -
2221 GAGGTAGCACTACAAACACAATATTCAAATCCAAATTCAAGCATTATTGAAATTGTAAGTG 2280
C -
2281 AAGTAAAACCTTAAGATAATTGAGTTAACCTTAAAGAATTAAATTTGGCATTTGTAC 2340
C -
2341 TAATACGGGAACATGAAGCCAGGTGTGGTGGTATGTACCTGTAGTCCCCAGGCTGAGGCC 2400
C -
2401 AGAGAATTACTTGAGCCCAGGAGTTGAATCCATCCTGGGCAGGATACTGGAGACCCCTGCC 2460
C -
2461 TTAAAAACXXAACAGXACCAAAACACCCAGGGACACATTTCTGTCTTTTGAT 2520
C -

HUMAN hiap-1

Fig. 2H

HUMAN hiap-2

SEQ ID NO:7 1 TTAGGTTACCTGAAAGAGTTACTACAACCCCAAAAGAGTTGTGTCTAAGTAGTATCCTGG 60
a -

61 TAATTCAAGAGATACTCATCCTACCTGAATAATAAACTGAGATAAAATCCAGTAAAGAAAG 120
a -

121 TGTAGTAATTCTACATAAGAGTCTATCATTGATTTCCTTGTGGAAATCTTAGTT 180
a -

181 CATTGTGAAGAAATTTCATGTGAATGTTTAGCTATCAAACAGTACTGTACCTACTCATG 240
a M -

241 CACAAAACCTCCCAAAGACTTTTCCCAGGTCCCTCGTATCAAAACATTAAAGAGTATA 300
a H K T A S Q R L F P G P S Y Q N I K S I -

301 ATGGAAGATAGCACGATCTTGTCAGATTGGACAAACAGCAACAAACAAAAATGAAGTAT 360
a M E D S T I L S D W T N S N K Q K M K Y -

16/61

Fig. 3A

HUMAN hiap-2

| | | | | |
|-----|---|---|---|-----|
| | | GACTTTTCTGTGAACTCTACAGAATGTCTACATATTCAACTTCCCCGGGGTGCCT | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - - + + - | 420 |
| 361 | a | D F S C E L Y R M S T Y S T F P A G V P - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | | GTCTCAGAAAGGAGTCCTTGCTCGTGCTGGTTTATATACTGGTGTGAATGACAAGGTC | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | 480 |
| 421 | a | V S E R S L A R A G F Y Y T G V N D K V - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | | AAATGGCTTCCTGTTGGCCCTGATGGCTGGATAACTGGAAACTAGGGAGACAGTCCTATTCAA | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | 540 |
| 481 | a | K C F C C G L M L D N W X L G D S P I Q - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | | AAGCATAAACAGCTATATCCTAGCTGTAGCTTATTCAAGAATCTGGTTTCAGCTAGTCTG | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | 600 |
| 541 | a | K H K Q L Y P S C S F I Q N L V S A S L - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | | GGATCCACCTCTAAGAATAACGTCTCCAATGAGAAACAGTTGGCACATTCAATTCTCCC | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | 660 |
| 601 | a | G S T S K N T S P M R N S F A H S L S P - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | | ACCTTGGAAACATAGCTGTTCAGTGGTCTTACTCCAGCCTTCCTCCAAACCCCTCTT | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | 720 |
| 661 | a | T L E H S S L F S G S Y S S L P P N P L - | - - - + + - - + - - + + - - + + - - + + - - + + - - + + - | |
| | a | | | |

17/61

Fig. 3B

HUMAN hiap-2

| | | |
|------|---|---|
| | AATTCTAGGCCAGTTGAAGACATCTCTCATCGAGGACTAACCCCTACAGTTATGCAATG | 780 |
| 721 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | N S R A V E D I S S S R T N P Y S Y A M | - |
| | AGTACTGAAAGAACGCCAGATTCTACCATATGTGGCCATTAACTTTTGTCACCA | 840 |
| 781 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | S T E E A R F L T Y H M W P L T F L S P | - |
| | TCAGAATTGGCAAAGAGCTGGTTTTATTATAGGACCTGGAGATAGGGTAGCCTGCTTT | 900 |
| 841 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | S E L A R A G F Y Y I G P G D R V A C F | - |
| | GCCCTGGGTGGGAAGGCTCAGTAACCTGGGAACCCAAGGGATGATGCTATGTCAGAACACCGG | 960 |
| 901 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | A C G G K L S N W E P K D D A M S E H R | - |
| | AGGCATTTCCCACACTGTCCATTGGAAAATTCTCTGAGGTTAGCATT | 1020 |
| 961 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | R H F P N C P F L E N S L E T L R F S I | - |
| | TCAAATCTGAGCATGCCAGACACATGGCTCGAACATTATGTAAGTGGCCATCT | 1080 |
| 1021 | - - - +-----+-----+-----+-----+-----+-----+-----+-----+-----+ | +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ |
| a | S N L S M Q T H A A R M R T F M Y W P S | - |

Fig. 3C

HUMAN hiap-2

19/61

| | | | | | |
|--|---|--|--|--|---|
| 1081 AGTGTCCAGTTCAGCCCTGAGCAGCTTGCAAGTGGCTGGTTATTATGTGGTCGCAAT a S V P V Q P E Q L A S A G F Y V G R N - | 1140 +-----+-----+-----+-----+-----+-----+ a GATGATGTCAAATGCTTGGTTGTGATGGCTTGAGGTGTTGGGAATCTGGAGATGAT 1141 +-----+-----+-----+-----+-----+-----+ a D D V K C F G C D G G L R C W E S G D D - | 1200 +-----+-----+-----+-----+-----+-----+ a CCATGGGTAGAACATGCCAAGTGGTTCCAAGGGTGGAGTTCTTGATACGAATGAAAGGC 1201 +-----+-----+-----+-----+-----+-----+ a P W V E H A K W F P R C E F L I R M K G - | 1260 +-----+-----+-----+-----+-----+-----+ a CAAGAGTTGTTGATGGAGATTCAAGGTAGATAATCCTCATCTTGAACAGCTGGTTGTCA 1261 +-----+-----+-----+-----+-----+-----+ a Q E F V D E I Q G R Y P H L L E Q L L S - | 1320 +-----+-----+-----+-----+-----+-----+ a ACTTCAGATACCAACTGGAGAAGAAAATGGCTGACCCACCAATTATTCAATTGGACCTGGA 1321 +-----+-----+-----+-----+-----+-----+ a T S D T T G E E N A D P P I I H F G P G - | 1380 +-----+-----+-----+-----+-----+-----+ a GAAAGTCTTCAGAAGATGGCTGTCATGATGAATAACACCTGTGGTTAAATCTGCCTTGAA 1381 +-----+-----+-----+-----+-----+-----+ a E S S S E D A V M M N T P V V K S A L E - |
|--|---|--|--|--|---|

Fig. 3D

HUMAN hiap-2

20/61

| | | | |
|------|---|--|---|
| 1441 | - | ATGGGCTTTAATAAGACCTGGTGAACAAACAGTTCTTAAGTAAAATCCTGACAACACTGGA | +-----+-----+-----+-----+-----+-----+-----+ |
| 1501 | - | GAGAACTATAAACAGTTAATGATATTGTGTCAGCACTTCTTAATGCTGAAGATGAAAAA | +-----+-----+-----+-----+-----+-----+-----+ |
| 1561 | - | AGAGAAGAGGAGAAGGAAAAACAAAGCTGAAGGAATGGCATCAGATGATTGTCAATTAAATT | +-----+-----+-----+-----+-----+-----+-----+ |
| 1621 | - | CGGAAGAACAGAATGGCTCTTCAACAAATTGACATGTGTGCCTATCCTGGATAAT | +-----+-----+-----+-----+-----+-----+-----+ |
| 1681 | - | CTTTAAAGGCCAATGTAATTAAATAACAGGAACATGATATTAAACAAAAACACAG | +-----+-----+-----+-----+-----+-----+-----+ |
| 1741 | - | ATACCTTACAAGGGAGAGAACTGATTCGATTCGGTTAAAGGAAATGCTGGGCC | +-----+-----+-----+-----+-----+-----+-----+ |
| a | M G F N R D L V K Q T V L S K I L T T G - | +-----+-----+-----+-----+-----+-----+-----+ | |
| a | E N Y K T V N D I V S A L L N A E D E K - | +-----+-----+-----+-----+-----+-----+-----+ | |
| a | R E E K E K Q A E E M A S D D L S L I - | +-----+-----+-----+-----+-----+-----+-----+ | |
| a | L L K A N V I N K Q E H D I I K Q K T Q - | +-----+-----+-----+-----+-----+-----+-----+ | |
| a | I P L Q A R E L I D T I W V V K G N A A A A - | +-----+-----+-----+-----+-----+-----+-----+ | |

Fig. 3E

HUMAN hiap-2

| | | |
|---|--|------|
| | AACATCTCAAAACTGTCCTAAAGAAATTGACTCTACATTGTATAAGAACATTATTGTG | 1860 |
| a | N I F K N C L K E I D S T L Y K N L F V - | 1861 |
| | GATAAGAATATGAAGTATATTCCAACAGAAGATGTTTCAGGCTCTGTCACTGGAAAGAACAA | 1920 |
| a | D K N M K Y I P T E D V S G L S L E E Q - | 1921 |
| | TTGAGGAGGTGGCAAGAAGAACGAACTTGTAAGTGTATGGACAAAGAACAGTTCTGTT | 1980 |
| a | L R R L Q E E R T C K V C M D K E V S V - | 1981 |
| | GTATTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCTCTCTAAGAAAA | 2040 |
| a | V F I P C G H L V V C Q E C A P S L R K - | 2041 |
| | TGCCCTATTGCAGGGGTATAATCAAGGGTACTGTTACATTCTCTCTAAAGAAAA | 2100 |
| a | C P I C R G I I K G T V R T F L S * - | 2101 |
| | ATAGTCTATATTAACTGGCATAAAAGGTCTTAAATATTGTGAACACTTGAGCC | 2160 |
| a | - | - |

Fig. 3F

HUMAN hiap-2

2161 ATCTAAAGTAAAAGGGAATTATGAGTTTCAATTAGAACATTCAATGGTCTAGTCTGC + 2220
a -
2221 TTTGGTACTAATAATCTTGTTCGAAAAGATGGTATCATATAATTAAATCTTAATCTGTT + 2280
a -
2281 TATTACAAAGGGAAAGATTATGTTGGTGAACCTATTAGTAGTATGTGTACCTAACGGG + 2340
a -
2341 AGTAGCGTCXCTGCTTGTATGCATCATTCAAGGAGTTACTGGATTGGTTGTTCTTCAG + 2400
a -
2401 AAAGCTTGAAXACTAAATTATAGTGTAGAAAAAGAACCTGGAAACCAGGAACTCTGGAGTT + 2460
a -
2461 CATCAGAGTTATGGTGCCGAATTGTCTTGCCTTTCACTTGTGTTAAATAAGGA + 2520
a -
2521 TTTCCTCTTATTCTCCCCCTAGTTGTGAGAACATCTCAATAAGTGCTTAAAGG + 2580
a -

Fig. 3G

MOUSE xiap

SEQ ID NO:9 1 GACACTCTGGCTGGGGGGCGCCCTCCGGACCTCCCTCGGGAACCGTCGCC 60
 a GCGGGCGCTTACAGTTAGGAACTGGAGTGCTTGGGGAAAAGGTGGACAAGTCCTATTTC 61 120
 a GAGAAGATGACTTTAACAGTTGAAGGAACTAGAACTTGTACTGGAGACACCAAT 121 180
 M T F N S F E G T R T F V L A D T N -
 AAGGATGAAGAATTGTAGAAAGAGTTAATAGATAAAACATTGCTAACTTCCAAAGT 181 240
 K D E E F V E E F N R L K T F A N F P S -
 AGTAGCTCCTGTTCAAGCATCAACATGGCGGAGCTGGTTCTTATACGGTGAAAGGA 241 300
 S S P V S A S T L A R A G F L Y T G E G -
 GACACCGTGCATGTTCAAGTTGCTATGGGGCAATAGATAGATGGCAAGTATGGGACTCA 301 360
 a D T V Q C F S C H A A I D R W Q Y G D S -

23/61

Fig. 4A

MOUSE xiap

24/61

| | | |
|-----|---|-----|
| 361 | GCTGTTGGAAAGACACAGGAGAATATCCCCAAATTGCGAGATTATCAAATGGTTTATT | 420 |
| a | A V G R H R R I S P N C R F I N G F Y F - | |
| | GAAATGGTGTGGCACAGTCTACAAATCCTGGTATCCAAAATGGCCAGTACAATCTGAA | |
| 421 | | 480 |
| a | E N G A A Q S T N P G I Q N G Q Y K S E - | |
| | AACTGTGTGGAAATAGAAATCCTTTGCCCTGACAGGCCACCTGAGACTCATGCTGAT | |
| 481 | | 540 |
| a | N C V G N R N P F A P D R P P E T H A D - | |
| | TATCTCTTGAGAACCTGACAGGTTGAGATATTCAAGACACCATATAACCCGAGGAACCC | |
| 541 | | 600 |
| a | Y L L R T G Q V V D I S D T I Y P R N P - | |
| | GCCATGTGTAGTGAAGTCATTCAAGACTATGCTCAT | |
| 601 | | 660 |
| a | A M C S E E A R L K S F Q N W P D Y A H - | |
| | TTAACCCCCAGAGAGTTAGTGTGGCCTCTACTACACAGGGCTGATGATCAAGTG | |
| 661 | | 720 |
| a | L T P R E L A S A G L Y Y T G A D D Q V - | |

Fig. 4B

MOUSE xiap

| | | |
|------|---|------|
| | CAATGCTTTGTTGTGGGGAAACTGAAAATTGGGAACCCCTGTGATCGTGCCTGGTCA | 780 |
| 721 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + - - - + | |
| a | Q C F C C G G K L K N W E P C D R A W S - | |
| | GAACACAGGAGACACTTCCCCAATTGCTTTGGGGAAACGTTAACGTTCA | |
| 781 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + | 840 |
| a | E H R R H F P N C F F V L G R N V N V R - | |
| | AGTGAATCTGGTGTGAGTTCTGATAAGGAATTTCACAAACTCTCCAAGAAAT | |
| 841 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + | 900 |
| a | S E S G V S S D R N F P N S T N S P R N - | |
| | CCAGCCATGGCAGAATATGAAGCACGGATCGTTACCTTTGGAACATGATACTCAGTT | |
| 901 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + | 960 |
| a | P A M A E Y E A R I V T F G T W I Y S V - | |
| | AACAAGGAGCAGCTTGCAGAGCTGGATTITATGCTTITAGGTGAAGGCCATAAAGTGAAG | |
| 961 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + | 1020 |
| a | N K E Q L A R A G F Y A L G E G D K V K - | |
| | TGCTTCCACTGTGGAGGGCTCACGGATTGGAAAGCCAAGTGAAAGACCCCTGGGACCAG | |
| 1021 | - - - - + - - - + - - + - - - + - - - + - - - + - - - + | 1080 |
| a | C F H C G G G L T D W K P S E D P W D Q - | |

Fig. 4C

MOUSE xiap

| | | | |
|------|---|------------------------------------|--------|
| | CATGCTAAGTGGTACCCAGGGTGC | AAATAACCTATTGGATGACAAGGGCAAGAATATA | |
| 1081 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1140 |
| a | H A K C Y P G C K Y L L D E K G Q E Y I | - | |
| | ATATAATTCAATTAAACCCATCCACTTGAGGAATCTTTGGAAACTGGCTGAA | AAACA | |
| 1141 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1200 |
| a | N N I H L T H P L E E S L G R T A E K T | - | |
| | CCACCGCTAACTAACCAATTGATGATAACCAC | TCTCCAGAATCCTATGGTGC | AAAGCT |
| 1201 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1260 |
| a | P P L T K K I D D T I F Q N P M V Q E A | - | |
| | ATACGAATGGGATTAGCTTCAGGACCTTAAGAA | AAACAATGGAAAGAAAAAATCCAACAA | |
| 1261 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1320 |
| a | I R M G F S F K D L K K T M E E K I Q T | - | |
| | TCCGGGAGCAGCTATCACTTGAGGTCTGATTGGCAGATCTTGCTGAGTCAGAAA | | |
| 1321 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1380 |
| a | S G S S Y L S L E V L I A D L V S A Q K | - | |
| | GATAATAACGGGAGATGAGTCAGTCAAACTCATTCATTGCAGAAAGACATTAGTACTGAAGAG | | |
| 1381 | - - - - + - - - + - - - + | + - - - + - - - + - - - + | 1440 |
| a | D N T E D E S S Q T S L Q K D I S T E E | - | |

26/61

Fig. 4D

MOUSE xiap

Fig. 4E

MOUSE xiap

28/61

| | | | |
|------|---|---|------|
| 1801 | TAGCCAGTGGTTACTCGATTGAAACCTTAGACAGAGCATTATAAGCTTTCACAT | - | 1860 |
| a | GTATATTGGTAGTACACTGACTTGACTTCTATATGTAAGTGAATTCAACCTGCATGTT | - | 1920 |
| a | TCATTCGCTTTGCATTAAGCTTAACAAATTGGAGTGGTTCTGTATAAGCATGGAGATGTGATG | - | 1980 |
| a | GAATCTGCCCAATGACTTTAACATTGGCTTATTGTAACACCGAAAGAAACTGCCACGGCTG | - | 2040 |
| a | CTGGGAGGATAAAGATTGGTTAGATGCTCACTCTGTGTTAGGATTCTGCCATTAA | - | 2100 |

Fig. 4F

M-hiap-1

Fig. 5A

M-hiap-1

Fig. 5B

M-hiap-1

TTTGGGTGGGATGGGAACCTGAGCAACTGGAACTGGCTATGTCAGGCCAC + 840
781 F A C D G K L S N W E R K D D A M S E H -

CAGAGGCATTCCCGAGGTGCTTCTTALLKGACTTGGGTCAAGTCAGTCAGATAAC + 900
841 Q R H F P S C P F L K D L G Q S A S R Y -

ACTGTCTCTAACCTGAGCATGCCAGCACACCGCAGCCCCGTATTAGAACATTCTCAACTGG + 960
901 T V S N L S M Q T H A A R I R T F S N W -

CCTTCCTAGTGCACTAAGTTCAGGAACCTGGCAAGTGGGGCTTTTATTACAGGA + 1020
961 P S S A L V H S Q E L A S A G F Y Y T G -

CACAGTGATGATGTCAGTGTATTATGCTGTGATGGTGGGTGAGGTGGAAATCTGGA + 1080
1021 H S D D V K C L C C D G G I R C W E S G -

GATGACCCCTGGTGGAACATGCCAAGTGGTTCCAAGGTGTGAGTACTTGCTCAGAAC + 1140
1081 D D P W V E H A K W F P R C E Y L L R I -

AAGGCCAAGAAATTGTCAGCCAAAGTCAAGCTGGCTATCCTCATCTACTTGAGGCATA + 1200
1141 K G Q E F V S Q V Q A G Y P H L L E Q L -

31/61

Fig. 5C

M-hiap-1

Fig. 5D

M-hiap-1

33/61

| | |
|------|--|
| 1561 | TGCCCTCCTAAAGTGCAGGGCCATCACTGAAACAGGAGTGCATGGCTGTGAAACAGAAACCA |
| | C L L S A R A I T E Q E C N A V K Q K P - |
| 1621 | CACACCTTACAAAGCAAGGACACTGATTGATACTGTGTTAGCAAAGGAACACTGCAGCA |
| | H T L Q A S T L I D T V L A K G N T A A - |
| 1681 | ACCTCATTCAAGAAACTCCCTCGGGAAATTGACCCCTGCGTTACAGAGATATTTGTG |
| | T S F R N S L R E I D P A L Y R D I F V - |
| 1741 | CAACAGGACATTAGGAGTCCTTCCCACAGATGACATTGCAGCTCTACAAATGGAAAGAACAG |
| | Q Q D I R S L P T D D I A A L P M E E Q - |
| 1801 | TTGGGGCCCTCCCCGGAGGACAGAAATGTGTAAGTGTGTATGGACCCGAGGGTATCCATC |
| | L R P L P E D R M C K V C M D R E V S I - |
| 1861 | GTGTTCATTCCTGTGGCCATCTGGCTGTGCAAAAGACTGGCTCCCTCTGTGAGGAAG |
| | V F I P C G H L V V C K D C A P S L R K - |

Fig. 5E

M-hiap-1

M-hiop-2

SEQ ID NO:41 CTGTGGGAGATCTATTGTCCTAAAGTGGTGGAAACTCATCTGGAAACTTAAGCGGTCA
1 - +-----+-----+-----+-----+-----+-----+-----+ 60
 GAAATACTTAACTACTCATGGACAKRACTGTCTCCCAGAGACTCGCCCCAAGGTACCTTA
61 - +-----+-----+-----+-----+-----+-----+-----+ 120
 CACCCRAAAACTTAAACGTATAATGGAGAACAGGACACAAATCTTGTCAAATGGACAAAGGA
121 - +-----+-----+-----+-----+-----+-----+-----+ 180
 M E K S T I L S N W T K E -

SEQ ID NO:42 GAGCGAAGAAAAATGAAGTTGACTTTTGACTGTGAACCTACCGAATGTCTACATATTG
181 - +-----+-----+-----+-----+-----+-----+-----+ 240
 S E E K M K F D F S C E L Y R M S T Y S -

AGCTTTCCAGGGAGTTCCCTGTCTCAGAGGGAGTCTGGCTCGTGGCTTTATTAA
241 - +-----+-----+-----+-----+-----+-----+-----+ 300
 A F P R G V P V S E R S L A R A G F Y Y -

TACAGGTGTGAATGACAAGTCAAGTGCTTCTGCTGGCCTGATGTTGGATAACTGGAA
301 - +-----+-----+-----+-----+-----+-----+-----+ 360
 T G V N D K V K C F C C G I M L D N W K -

ACAAGGGGACAGTCCTGTGAAAGCACAGACAGTTCTATCCCAAGCTGGAGCTTGTACA
361 - +-----+-----+-----+-----+-----+-----+-----+ 420
 Q G D S P V E K H R Q F Y P S C S F V Q -

Fig. 6A

M-hiap-2

421 GACTCTGCTTTCAGCCAGTCTGCAGTCTCATTAGAATAATGTCTCCTGTGAAAAGTAG
421 T L S A S L Q S P S K N M S P V K S R - 480

481 ATTCACATTCTGTCACTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC
481 F A H S S P L E R G G I H S N L C S S P - 540

541 TCTTAATTCTAGGCGAGTGGAAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT
541 L N S R A V E D F S S R M D P C S Y A M - 600

601 GAGTACAGAAGAGGCCAGATTCTTACTAACGTTAGTGGCCTTTAACGTTTCTGTCAACC
601 S T E E A R F L T Y S M W P L S F L S P - 660

661 AGCAGAGCTGGCCAGAGCTGGCTCTATTACATAGGGCCTGGAGACAGGGTGGCCTGTT
661 A E L A R A G F Y Y I G P G D R V A C F - 720

721 TGCCCTGTGGTGGAAACGTGAGCAACTGGGAACCAAAGGATTATGCTATGTCAGAGCACCG
721 A C G G K L S N W E P K D Y A M S E H R - 780

Fig. 6B

M-hiap-2

| | | | | | |
|---|--|---|---|--|---|
| CAGACATTTCCCCACTGTCCATTCTGGAAAATACTTCAGAAACACAGAGTTAGTAT 781 - - - + - - + - - + - - + - - + - - + - - + - - + - - + 840 | ATCAAATCTAAGGATGCCAGACACACTCTGCCTGAGGACATTTCTGTACTGGCCACC 841 - - - + - - + - - + - - + - - + - - + - - + - - + - - + 900 | TAGTGTTCCTGTTCAAGCCCCGAGCGCAAGTGCTGGATTACGTGGATCGCRA 901 - - - + - - + - - + - - + - - + - - + - - + - - + 960 | TGATGATGTCAGTGCCTTGTGATGGCTGGCTTGAGATGTTGGAACCTGGAGATGA 961 - - - + - - + - - + - - + - - + - - + - - + - - + 1020 | CCCCTGGATAGAACACGCCAAATGGTTCCAAAGGTGTGAGTTCTTGATACGGATGAGGG 1021 - - - + - - + - - + - - + - - + - - + - - + 1080 | TCAGGAGTTTGTGATGAGATTCAAGCTAGATAATCCTCATCTTGAGCAGCTGTGTC 1081 - - - + - - + - - + - - + - - + - - + - - + 1140 |
| R H F P H C P F L E N T S E T Q R F S I - | S N L S M Q T H S A R L R T F L Y W P P - | S V P V Q P E Q L A S A G F Y Y V D R N - | D D V K C L C C D G G L R C W E P G D D - | P W I E H A K W F P R C E F L I R M K G - | Q E F V D E I Q A R Y P H L L E Q L L S - |

Fig. 6C

M-hiap-2

CACTTCAGACACCCCAAGGAGAAGAAATTGGCTGACCCCTAACAGAGAACAGTGGTGCATTGG
1141 T S D T P G E E N A D P T E T V V H F G - +-----+ 1200

CCCTGGAGAAAGTTCGAAAGATGTCTCATGATGAGCACCGGCCCTGGTTAACAGGCCCT
1201 P G E S S K D V V M M S T P V V K A A L - +-----+ 1260

GGAAATGGGCTTCAGTAGGAGCCTGGTGGACAGACAGACGGTCAAGGGCAGATCCTGGCCAC
1261 E M G F S R S L V R Q T V Q R Q I L A T - +-----+ 1320

TGGTGAGAACTACAGGACCGTCAATGATAATTGTCCTCAGTACTTTGAATGCTGAAGATGA
1321 G E N Y R T V N D I V S V L L N A E D E - +-----+ 1380

GAGAAGAGAAAGGAGAAGGAAAGACAGACTGAAGAGATGGCATCAGGTGACTTATCACT
1381 R R E E K F R Q T E E M A S G D L S L - +-----+ 1440

GATTGGAAAGAATAGAATGGCCCTCTTCAACAGTTGACACATGTCCTCCATCCTGGA
1441 I R K N R M A L E Q Q L T H V L P I L D - +-----+ 1500

Fig. 6D

M-hiap-2

| | | |
|------|---|------|
| 1501 | TAATCTTCTTGAGGCCAAGTGTAAATTACAAAACAGGAACATGATATTAGACAGAAAC | 1560 |
| | N L L E A S V I T K Q E H D I I R Q K T - | |
| 1561 | ACAGATAACCCTTACAAGCAAGAGAGCTTATTGACACCGTTTAGTCAGGGAAATGCTGC | 1620 |
| | Q I P L Q A R E L I D T V L V K G N A A - | |
| 1621 | AGCCAACATCTCAAAACTCTCTGAAGGGAAATTGACTCCACGTTATATGAAAACCTATT | 1680 |
| | A N I F K N S L K G I D S T L Y E N L F - | |
| 1681 | TGTGAAAAGAATATGAAGTATATTCAACAGAACGTTICAGGCTTGTGATTGGAAAGA | 1740 |
| | V E K N M K Y I P T E D V S G L S L E E - | |
| 1741 | GCAGTTGGGAGATTACAGAACGAAACTTGCAAAGTGTGTATGGACAGAGGGTTTC | 1800 |
| | Q L R R L Q E E R T C K V C M D R E V S - | |
| 1801 | TATTGTTCATTTCCGGTGGTCAATCTAGTAGTGTGCCAGGAATGTGCCCTCTCTAAG | 1860 |
| | I V F I P C G H L V V C Q E C A P S L R - | |

Fig. 6E

M-hiap-2

Fig. 6F

Alignment of BIR (Baculoviral IAP Repeats) Domains

| | | | |
|---------------------------|--|------------------------------------|---|
| Baculovirus | | | |
| Cp_iap | Cydia pomonella | | |
| Op_iap | Orygia pseudotsugata | | |
| Human | | | |
| xiap | IAP on X chromosome | | |
| hiap1, hiap2 | two different human IAP genes | | |
| Mouse | | | |
| mi-xiap | mouse homologue of human xiap gene | | |
| Insect | | | |
| diap | Drosophila IAP gene, not clearly a homologue of xiap or hiap | | |
| note on consensus: | The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence. | | |
| | 1 | 68 | |
| SEQ ID NO:11 | Op_iap-1 | kaaRLGTYtn WPvqf..leps rMAasGTYYI | GrgDeVrCaf CkveitnWvr waPqCpFV |
| SEQ ID NO:14 | Cp_iap-1 | eevRlntFek WPvsf..lsp e | 41/61 GrsDeVrCaf CkveimrWke gEdpaaDHkk waPqCpFV |
| SEQ ID NO:15 | diap-2 | eanRLvTFkd WPnnp..lpq aLAkAGFYyI | ffPqCpRV |
| SEQ ID NO:16 | m-xiap-1 | efnRLkTfan FPsspsvas tLARAGFLYT | nDnafeeHkr CngviakWeK |
| SEQ ID NO:17 | xiap-1 | efnRLkTfan FPsgspvsas tLARAGFLYT | GedDtVqCFs ChaaidrWQY |
| SEQ ID NO:18 | hiap1-1 | elyRMstYST FPagvpvsr sLARAGFYyt | GedDtVrcFfS ChaavdrWQY |
| SEQ ID NO:19 | hiap2-1 | elyRMstYST FPagvpvsr sLARAGFYyt | GvndkVkcFc CgmldnWkr gDsptekHkk |
| SEQ ID NO:20 | m-xiap-2 | earRLksFqn WPdyahltpz elASAGLYYT | GvndkVkcFc CgmldnWkl gDspiqkhkq |
| SEQ ID NO:21 | xiap-2 | earRLksFqn WPdyahltpz elASAGLYYT | LyPsCsFI |
| SEQ ID NO:22 | hiap1-2 | enarLLTfqWP..lfslspt dLARAGFYyI | Cggk1knWep CDrawsErr |
| SEQ ID NO:23 | hiap2-2 | earRFITym WP..lfslsps elARAGFYyI | hfpncFFV |
| SEQ ID NO:24 | m-xiap-3 | yearIVTfgt Wiysv..nke qLARAGFYyI | hfpncFFV |
| SEQ ID NO:25 | xiap-3 | yearIfffgt Wiysv..nke qLARAGFYyI | cDrawsErr |
| SEQ ID NO:26 | hiap1-3 | haarFKTffn WPsssvlnpe qLAsAGFYyyV | hfpkCpFI |
| SEQ ID NO:27 | hiap2-3 | haarMRITfmy WPsssvpqpe qLAsAGFYyyV | hfdamseHlr |
| SEQ ID NO:28 | Op_iap-2 | earLrlTfae WPrqlkqrpe eLAeAGFFyt | Cggk1knWep |
| SEQ ID NO:29 | Cp_iap-2 | earRvksfnn WPrcmkqrpe qMADAGFFyt | Cggk1knWep |
| SEQ ID NO:30 | diap-3 | vdaRLrlTfTd WPisniqpas aLAqAGLYYq | GygdntkCFY |
| SEQ ID NO:31 | diap-1 | esvRLatFge WPlnapvsae dLvanGFF.. | K1gDqVrcFh |
| SEQ ID NO:2 | Consensus | --RL-TF-- WP----- | CnigrlsWqk |
| SEQ ID NO:3 | | -LA-AGFYy- G--D-V-CF- | eDepwieHak |
| SEQ ID NO:4 | | - - - - - D-----H-- | wsPkCqFV |
| SEQ ID NO:5 | | - - - - - W-- | ChvridrWey |
| SEQ ID NO:6 | | - - - - - P-C-FV | gDlvaerHrr |
| SEQ ID NO:7 | | | sspICsmV |
| SEQ ID NO:8 | | | |

Fig. 7

Fig. 8A

| | | | |
|-----|---|--|--|
| 200 | | | |
| 151 | cp-iap diap m-xiap xiap hiap1 hiap2 consensus | ...:esDnegnsvv ppEthadyll pSEthadyll ang... ave... -E- | ...:dsspescspd rtggvVDISD rtggvVDISD tiyprnp..AM ...:EfSa ...:DiSS -D-SD |
| 201 | cp-iap diap m-xiap xiap hiap1 hiap2 consensus | ...:PetMAKngFY PqalAkAGFY PRELASAGLY PRELASAGLY PtDLARAGFY PSELARAGFY P-ELA-AGFY | ...:Y1GrsDeVrC Y1nrlDhvKC YtGaddQvQC YtGigDQvQC YigpgDrvac YigpgDrvac Y-G-D-V-C |
| 250 | BIR 2 | | |
| 201 | cp-iap diap m-xiap xiap hiap1 hiap2 consensus | ...:afCKveimrW vwCnGviakW FCCGGKLKNW FCCGGKLKNW FaCGGKLSNW FaCGGKLSNW F-CGGKL-NW | ...:kegedpaADH EknDnAfEEH EpcDRAWSEH EpcDRAWSEH EPkDNAmSEH EPkDDAmSEH EP-D-A-SEH |
| 250 | BIR 3 | | |
| 251 | cp-iap diap m-xiap xiap hiap1 hiap2 consensus | kgidvcgssiv qmplie.fa Igrnnvnrse 1grnlnirse ...:... ...:... ...:... | httiigPaHP qpttl.PlrP pnStnsPrNP pnStnlPrNP tvs....N1 enqlqdtsry ensl.etlrf sis...N1 -S...-F |
| 250 | BIR 3 | | |
| 300 | | | |
| | | | |

8B
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BIR 3

| | 301 | 350 | 401 | 450 |
|-----------|-------------|------------|-------------|-------------|
| cp-iap | qrpeQMAdAG | FFYtGYGdnt | KCFYCdGGlk | dWepedDvPWe |
| diap | QpasallAqAG | LYYqk1Gdqv | rCFhcnIGlr | OHvrWFdrCa |
| m-xiap | VnkeQLARAG | FyAlGeGDKv | swqkedEPwf | EHAKWspKcq |
| xiap | VnkeQLARAG | FyAlGeGDKv | dWkpseDPwd | QHAKCYPgCK |
| hiap1 | VnpeQLASAG | FyYVGnsDdv | KCFhCggGLt | QHAKWypGCK |
| hiap2 | VqpeQLASAG | FYyVGRsDdv | KCFCCdgGLr | cWesgDDPwv |
| consensus | V--EQLA-AG | FYY-G-GD-V | KCF-C-GGL- | QHAKWFPrCe |
| | | | -W---DDPW- | QHAKWFp-C- |
| 351 | YvqlvKGrdY | VqkVit... | ...e..... | ... |
| cp-iap | FvllakGpay | VseVlattaa | nassqpaTap | aptlq..... |
| diap | YllideKGQEY | InnIhlthp. | LeEsLgrTae | kt..... |
| m-xiap | YlleqKGQEY | InnIhlths. | LeEcLvrTte | kt..... |
| xiap | YlirikGQEY | IrqVqasyph | LLEql11stSD | psltr |
| hiap1 | FJirmKGQEF | VdeIqgryph | spgdenaess | ihlepgedh |
| hiap2 | Yll---KGQEY | --- | ttgeenadpp | iihfgPgesS |
| consensus | | | P----- | |
| | | | L-E-L-T-- | |
| | | | | |

Fig. 8C

| | 451 | 500 | 501 |
|------------------|------------|------------|------------|
| cp-iap | | | |
| diap | fddagagaal | Evreppe.. | |
| m-xiap | vSAqkDntED | E..... | |
| xiap | vnAqkDsmqD | E..... | |
| hiap1 | lnAedEireE | Ererateeke | snndlirkn |
| hiap2 | lnAedEKreE | Erekqaeema | rmalfqhltc |
| consensus | -A----- | E----- | sddslirkn |
| | | | rmalfqqltc |
| | | | vlpidnlk |

| | 500 | 550 |
|------------------|------------|-----------------|
| cp-iap | | |
| diap | | psapfie |
| m-xiap | | pcqattskaa |
| xiap | | ssQtsLQ..... |
| hiap1 | aginneqehd | ssQtsLQ..... |
| hiap2 | anvinkqehd | vikqktQtsL |
| consensus | | Qarelidtil |
| | | vkgniaatvf |
| | | Qarelidtiw |
| | | vkgnaaaanif |
| | | knclkeidst |
| | | Q-----Q-LQ----- |

Fig. 8D

| | | Ring Zinc Finger | | | | | | | | | |
|-----------|------------|------------------|------------|------------|-------------|------------|-----|---|---|---|--|
| | | 551 | | | | | 600 | | | | |
| cp-iap | tki | qkmisvstping | nisiEEenrq | Ekepq | veDskLCKIC | yveEc1VCFV | | | | | |
| diap | sniskitdei | qkmisvstping | distEEenrq | LkDarLCKVC | LDeEVgVVVF1 | | | | | | |
| m-xiap | | | distEEQLR | LQEEKLsKIC | MDrnIaIVFF | | | | | | |
| xiap | | | eiSSEEQLR | LQEEKLCKIC | MDrnIaIVFV | | | | | | |
| hiap1 | lyehlfvqqd | ikyiptedvs | d1pveEQLR | LpeertCKVC | MDKEVSIVFI | | | | | | |
| hiap2 | lyknlfvdkn | mkyiptedvs | g1S1EEQLR | LqeerrCKVC | MDKEVSIVFI | | | | | | |
| consensus | - | - | - | - | - | - | - | - | - | - | |
| | | 601 | | | | | 635 | | | | |
| cp-iap | PCGHVVaCak | CA1SVdkCPM | OrkIVtsvlk | VYPS | | | | | | | |
| diap | PCGHLatCnq | CAPSVancPM | CradiKqfrv | tFLS* | | | | | | | |
| m-xiap | PCGHLatCkq | CAeaVdkCPM | CytVtFnqk | iFMS* | | | | | | | |
| xiap | PCGHLvtckq | CAeaVdkCPM | CytVtFkqk | iFMS* | | | | | | | |
| hiap1 | PCGHLVvckd | CAPS1rkCPi | CRstIkgtvr | tFLS* | | | | | | | |
| hiap2 | PCGHLVvCqe | CAPS1rkCPi | ORGIIkgtvR | tFLS | | | | | | | |
| consensus | PCGHLV-C- | CA-SV-KCPM | CR-I----- | -FLS- | | | | | | | |

Fig. 8E

Alignment of RZF (Ring Zinc Finger) Domains

| | |
|--------------------|---|
| Baculovirus | <i>Cydia pomonella</i> <i>Orygia pseudotsugata</i> |
| Human | IAP on X chromosome two different human IAP genes |
| Mouse | mouse homologue of human xiap gene |
| Insect | Drosophila IAP gene, not clearly a homolog |
| Cp_iap | xiap |
| Op_iap | hiap1, hiap2 |
| m-xiap | m-xiap |
| diap | diap |

note on consensus:

The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

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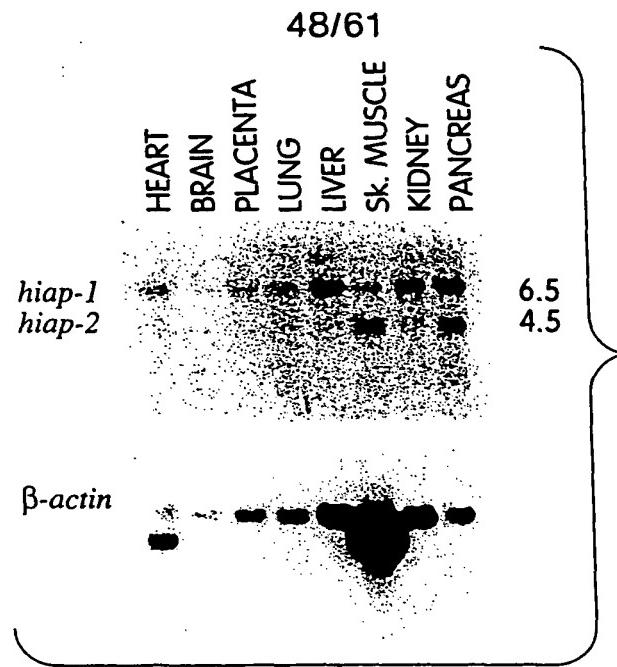


Fig. 10A

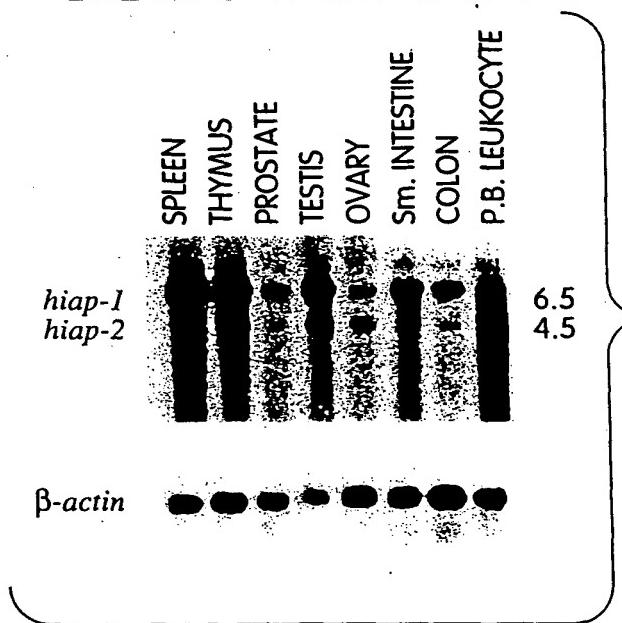


Fig. 10B

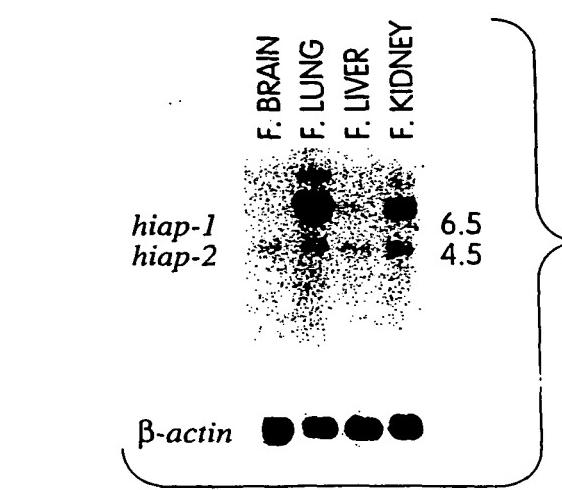


Fig. 10C

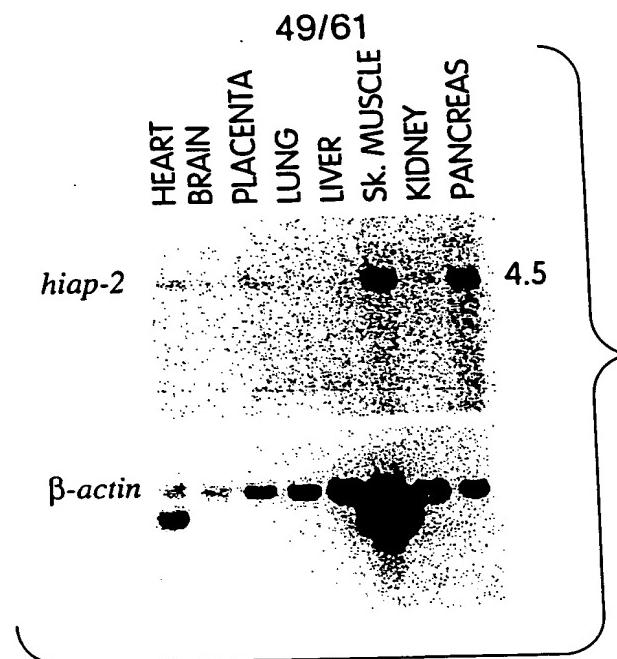


Fig. 11A

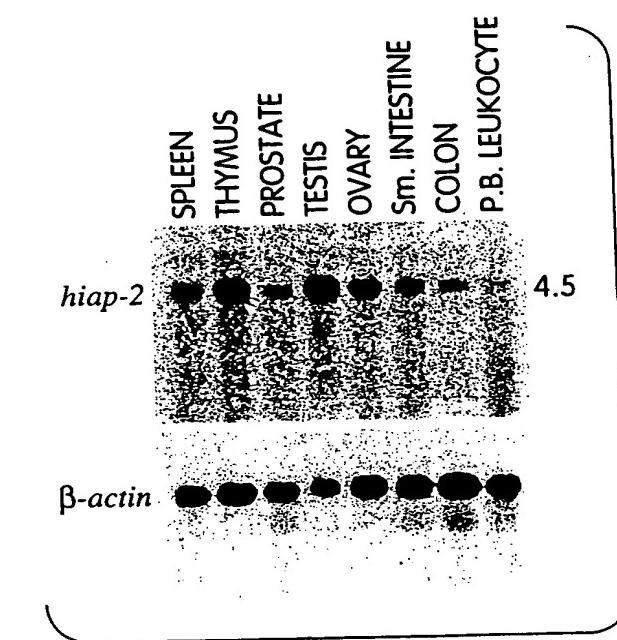


Fig. 11B

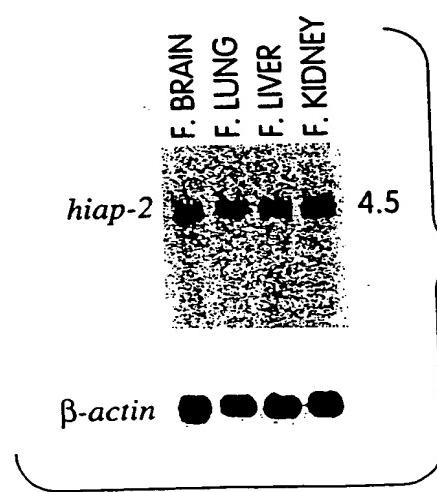


Fig. 11C

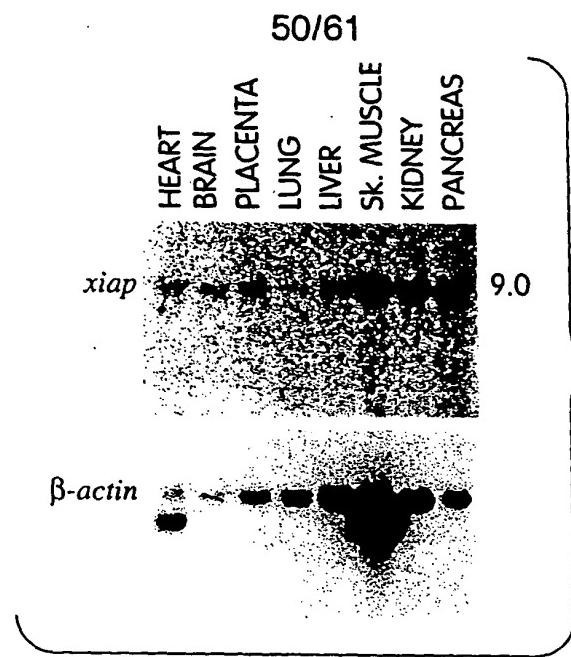


Fig. 12A

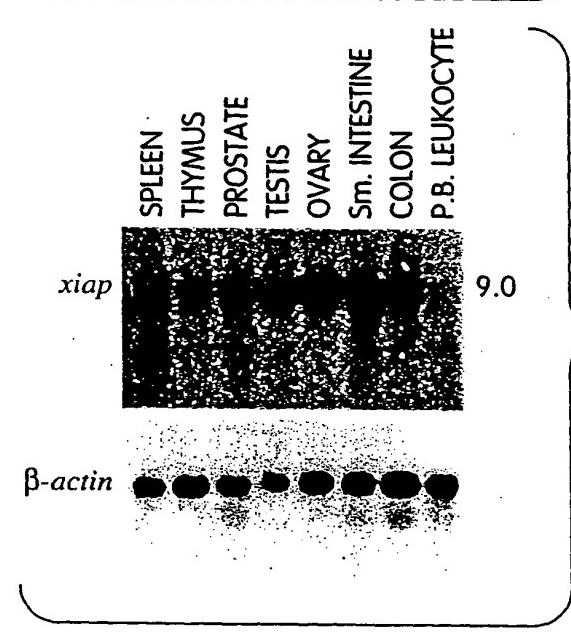


Fig. 12B

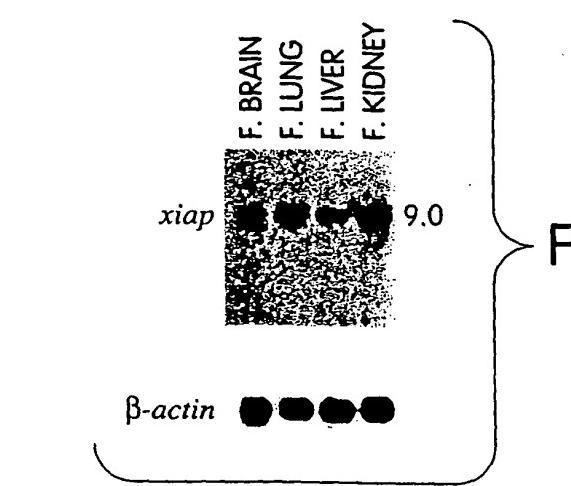


Fig. 12C

51/61

| S: STANDARDS | INCUBATION: OVERNIGHT | | | | | | | |
|--------------|-----------------------|---------------------|-------------|-------------|-------------|-------------|-------------|-------|
| | Hg | CEM-CM ₃ | GT/CEM | JKT | | | | |
| HIV | - - + | - - + | - - + | - - + | - - + | - - + | - - + | - - + |
| PHA/PMA | - + - - | + - - | - - + | - - + | - - + | - - + | - - + | - - + |
| S | + - - + - - | + - - + - - | + - - + - - | + - - + - - | + - - + - - | + - - + - - | + - - + - - | S |

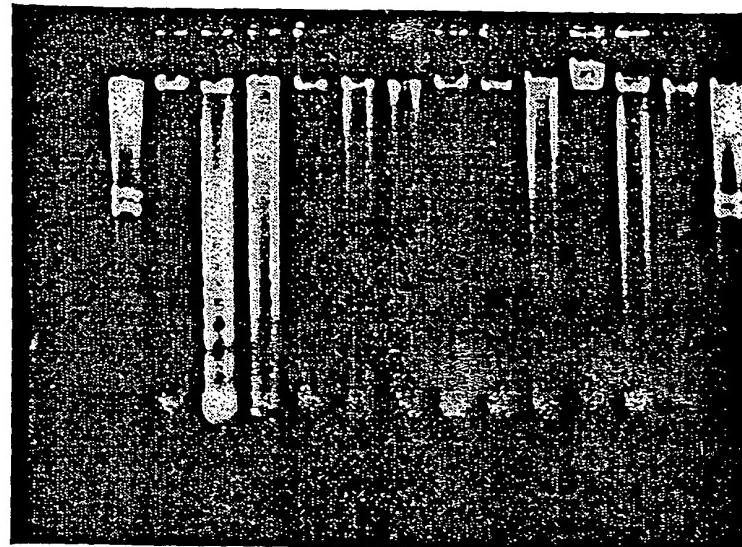


Fig. 13A

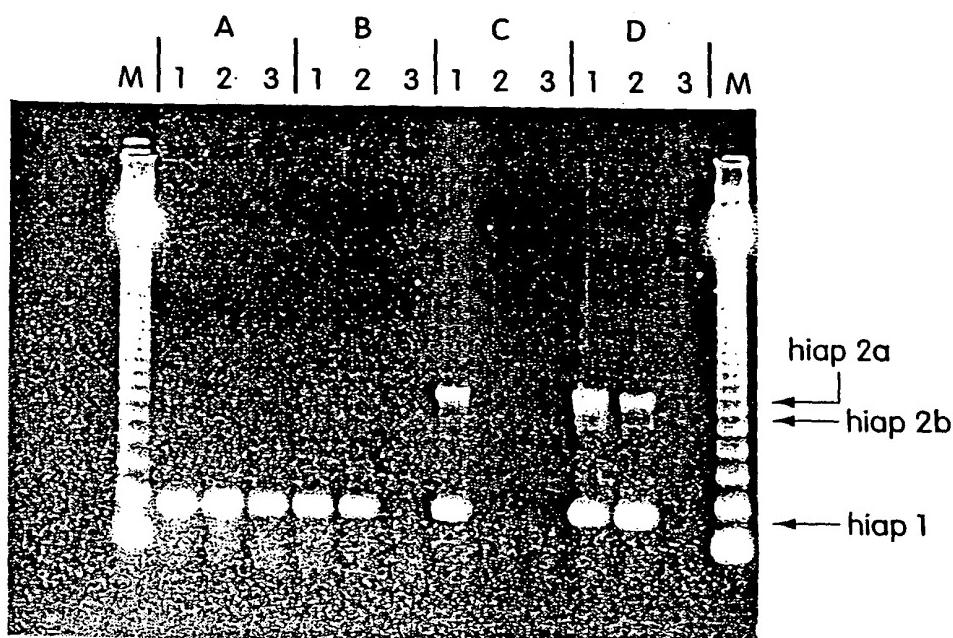


Fig. 13B

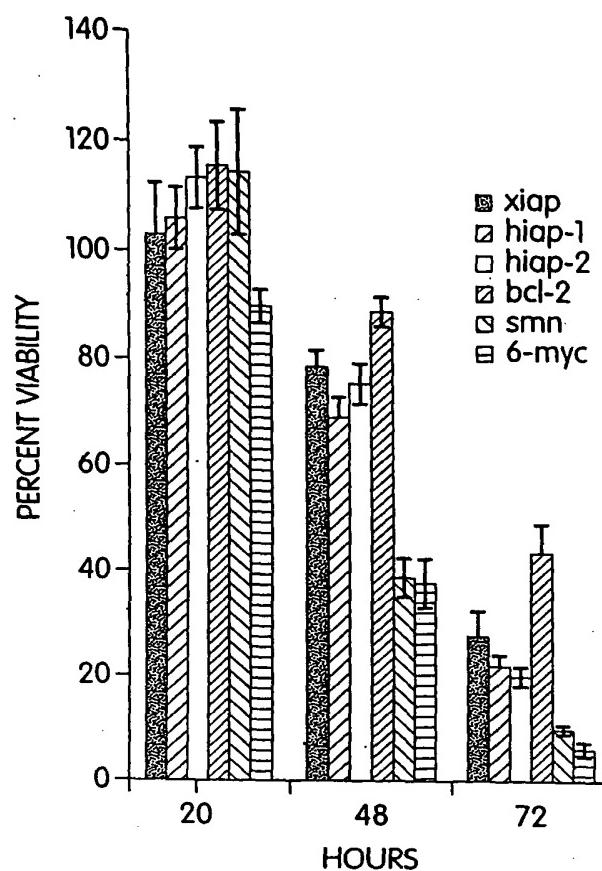


Fig. 14A

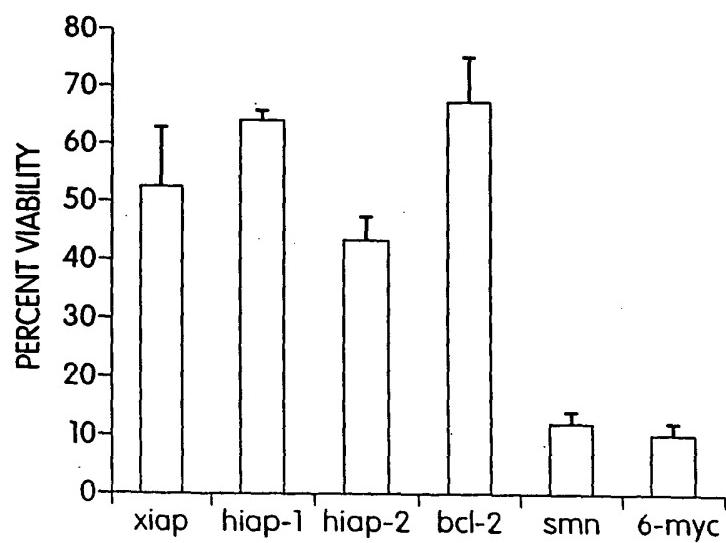


Fig. 14B

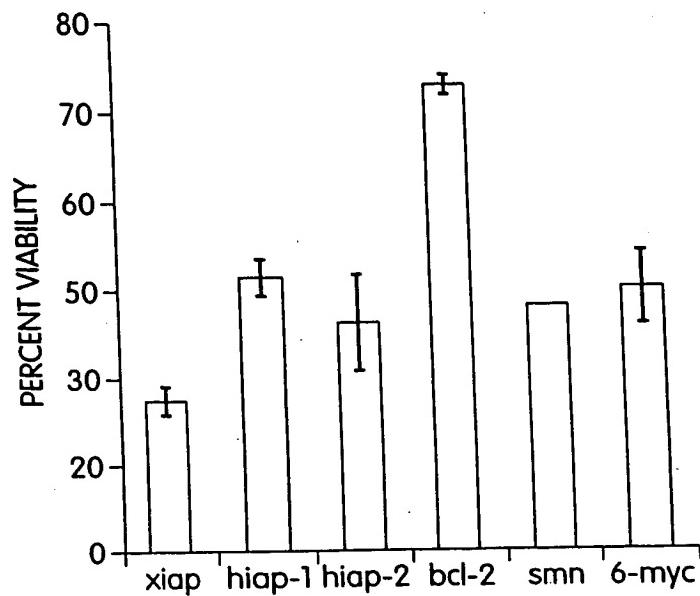


Fig. 14C

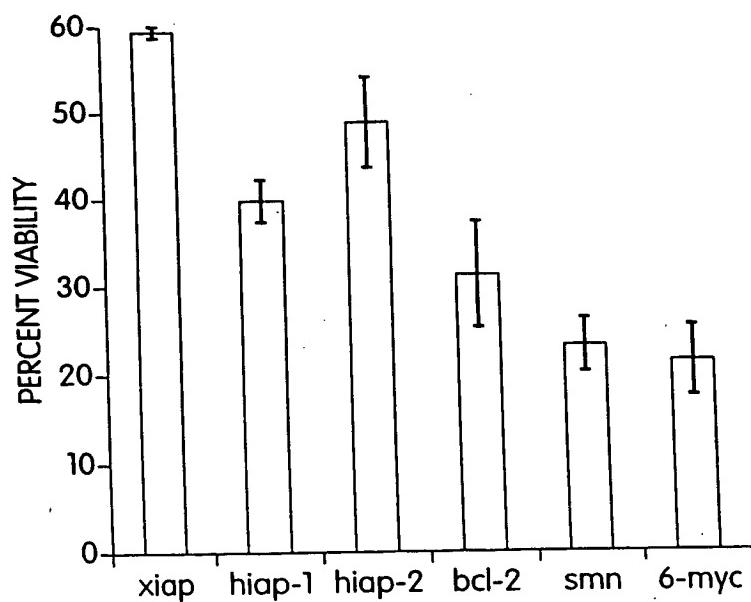
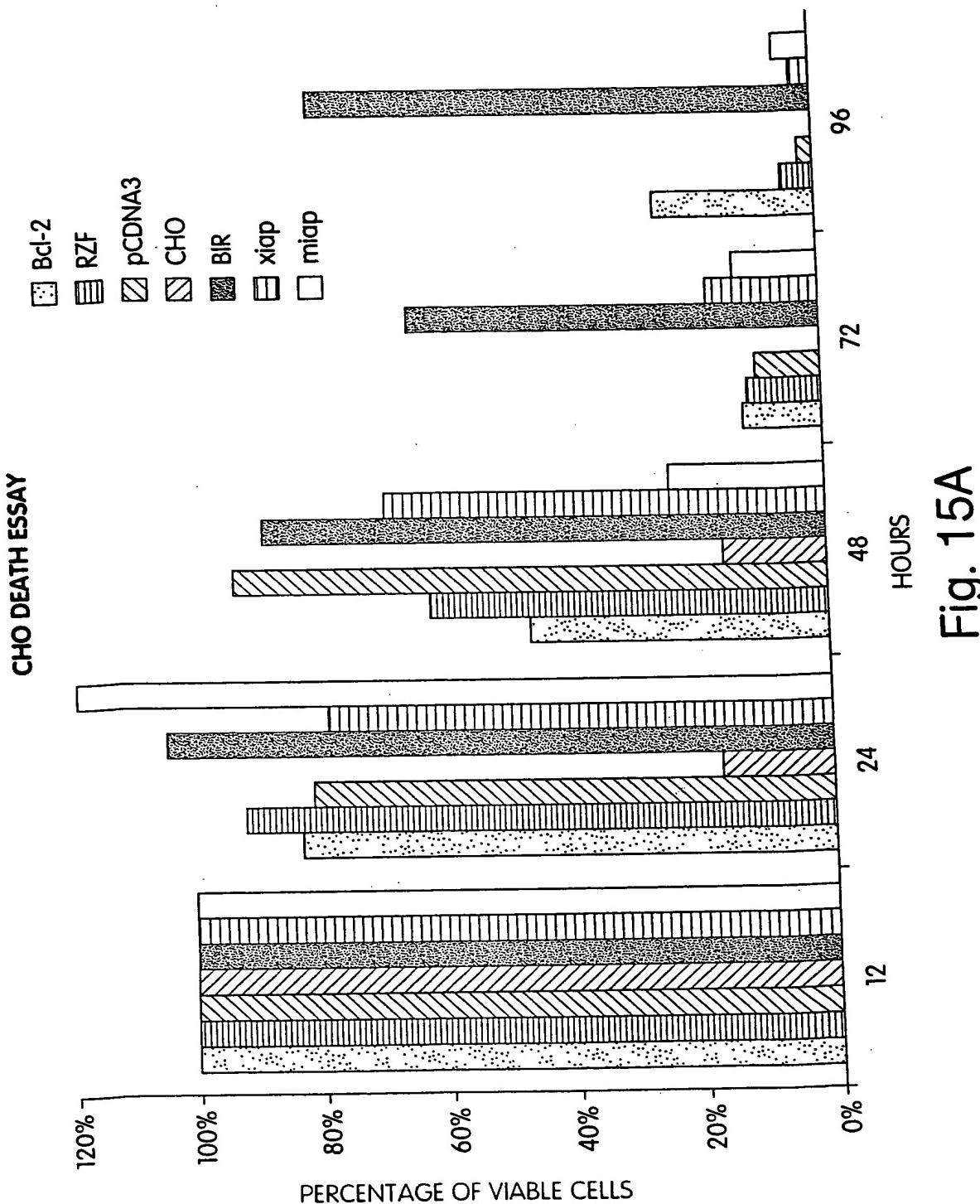
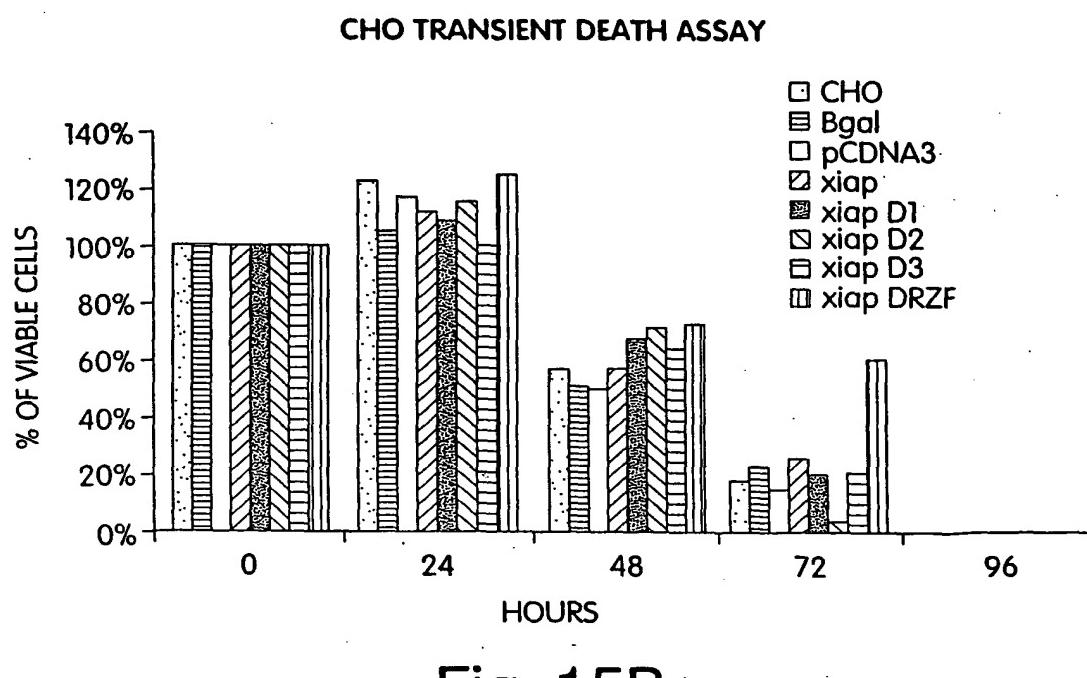
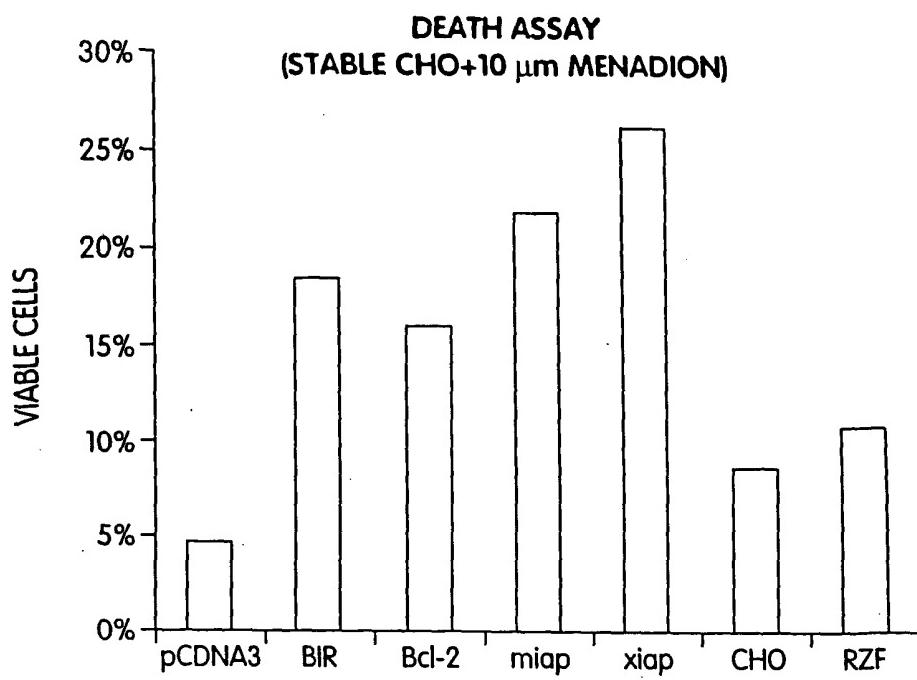
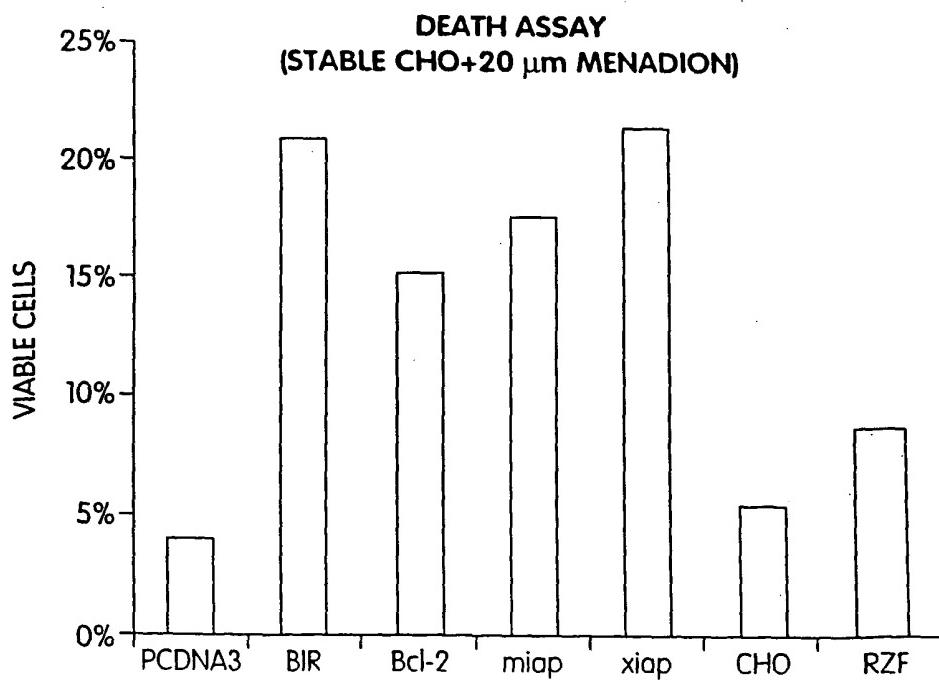


Fig. 14D





**Fig. 16A****Fig. 16B**

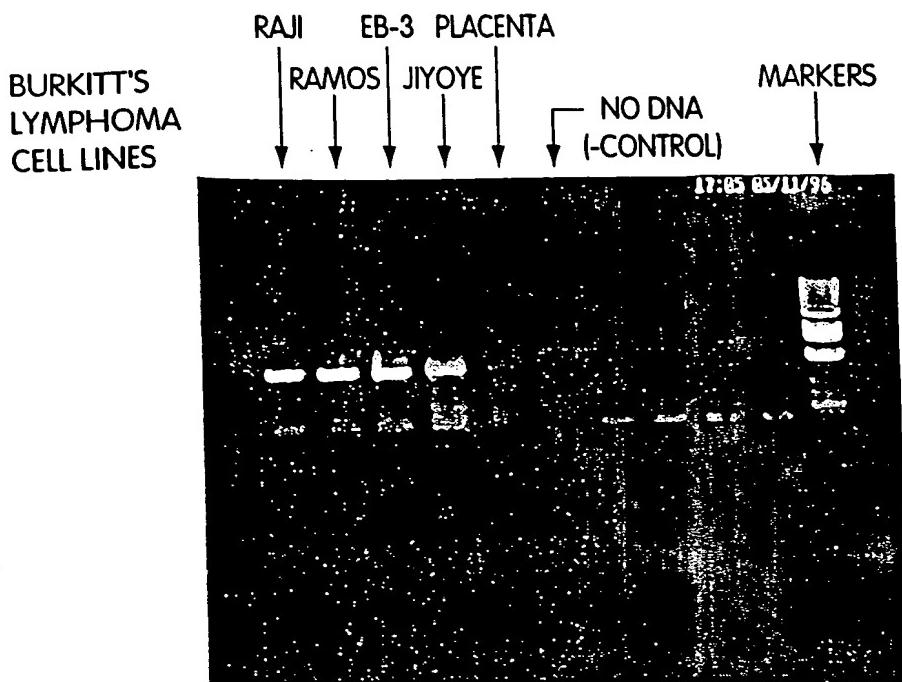


Fig. 17

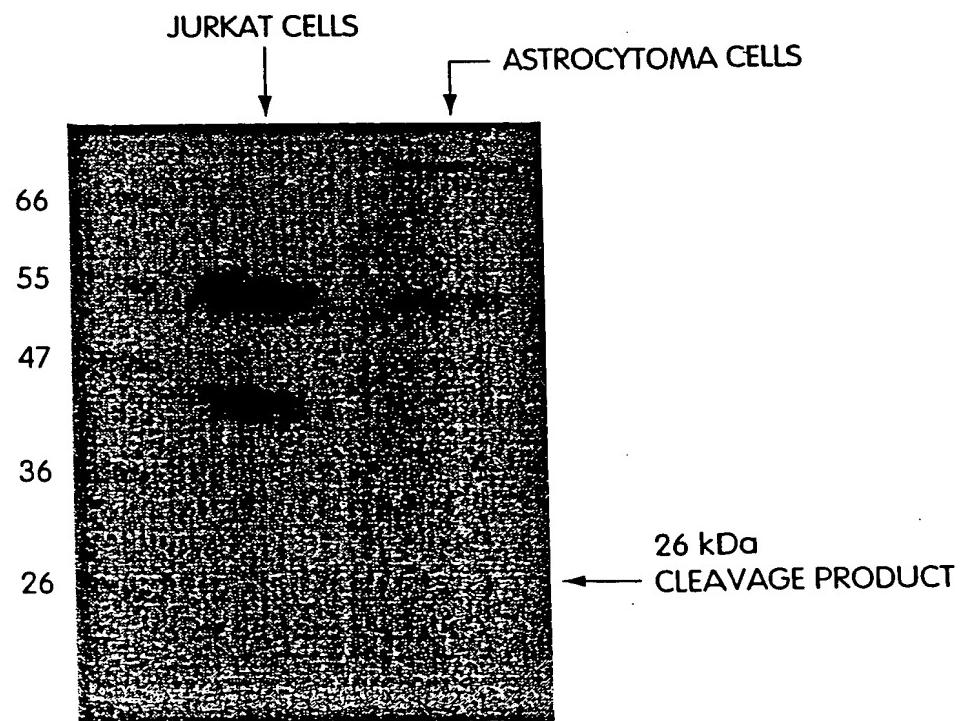


Fig. 18

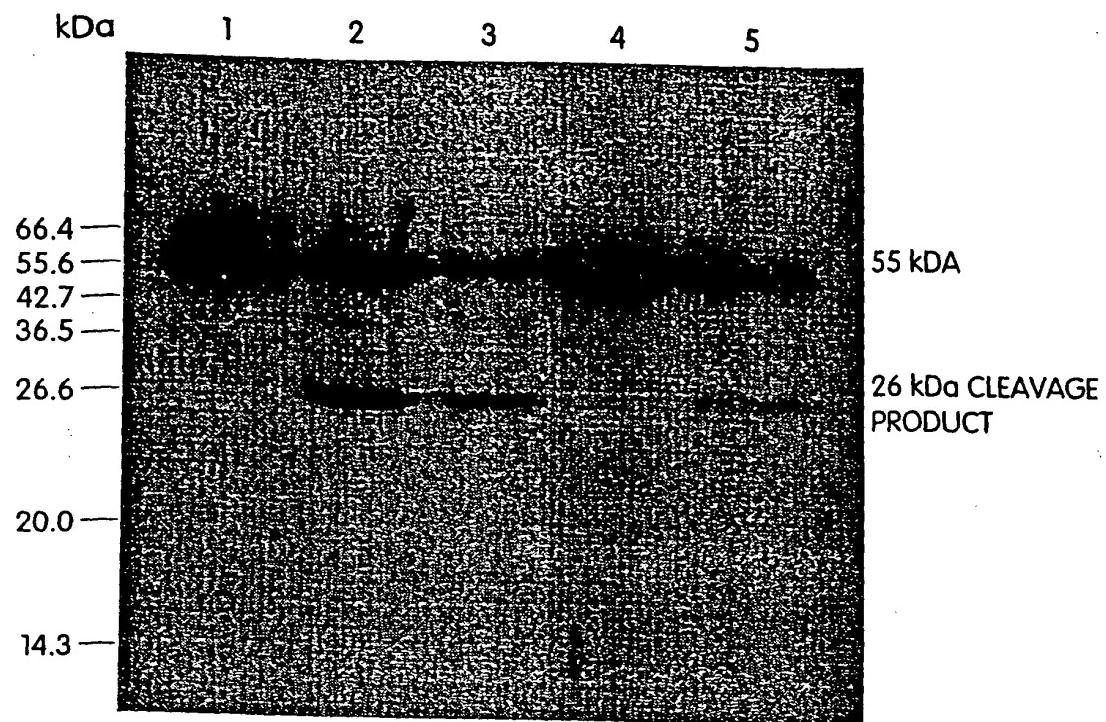


Fig. 19

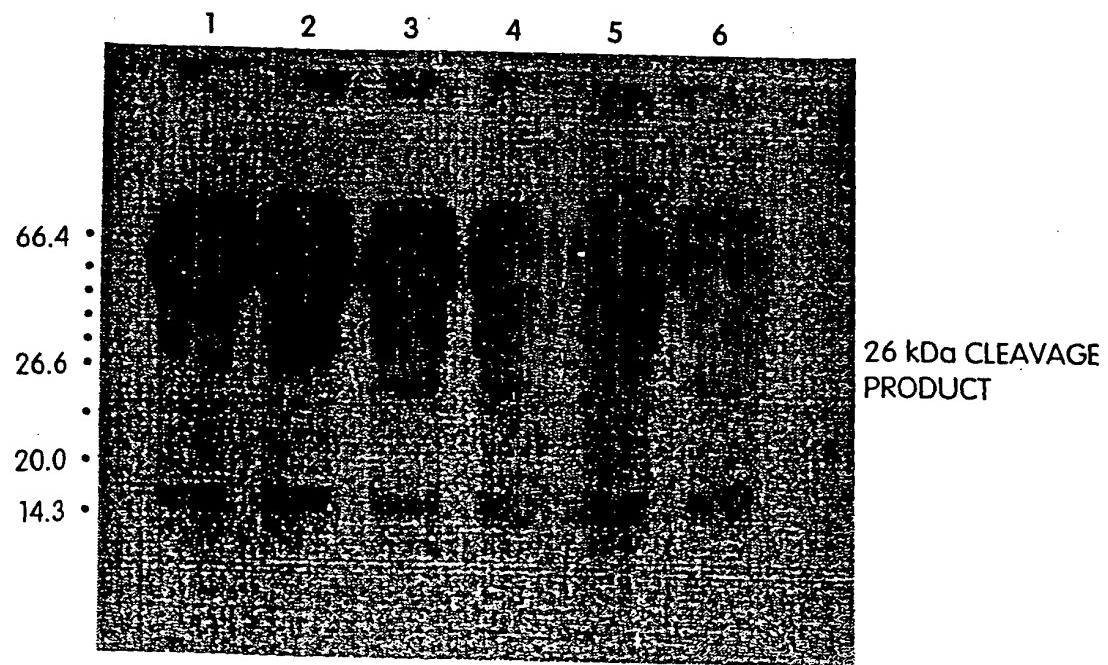


Fig. 20

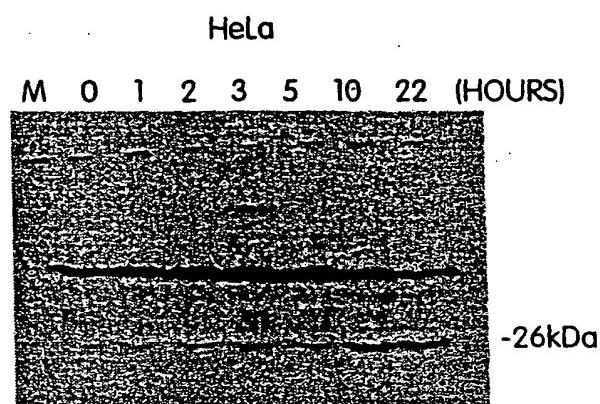


Fig. 21A

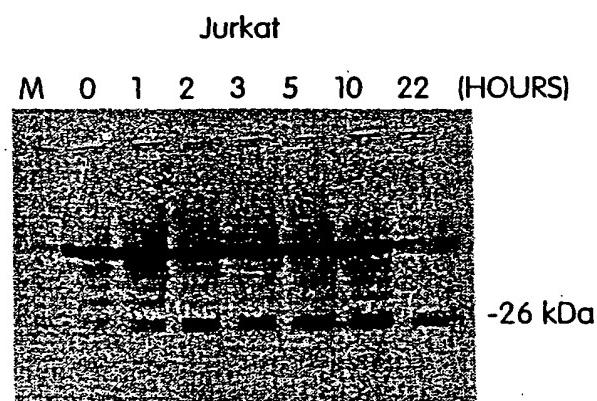


Fig. 21B

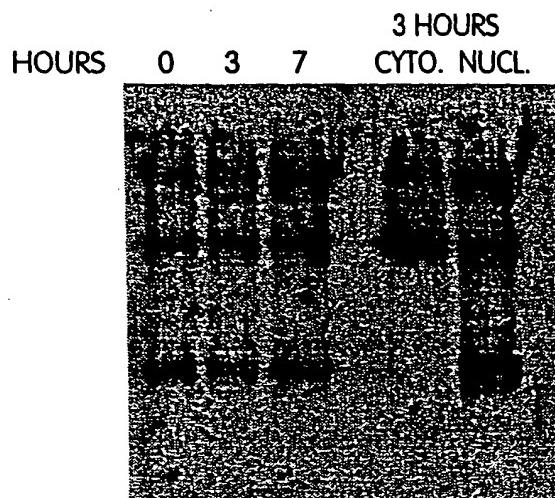


Fig. 22A

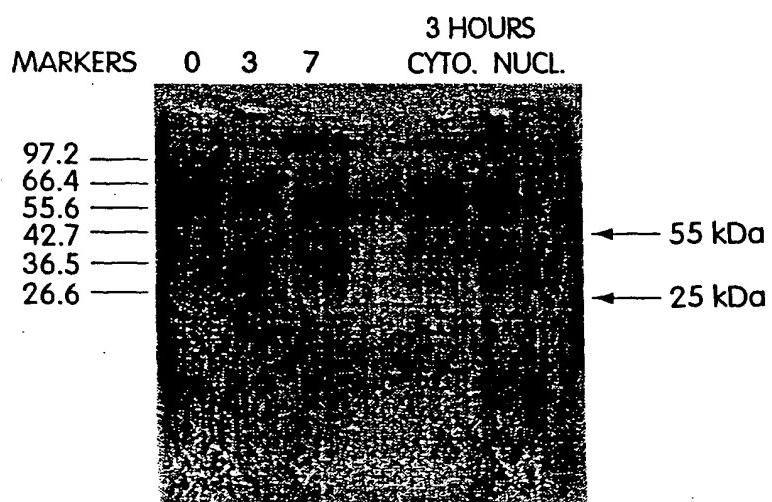


Fig. 22B

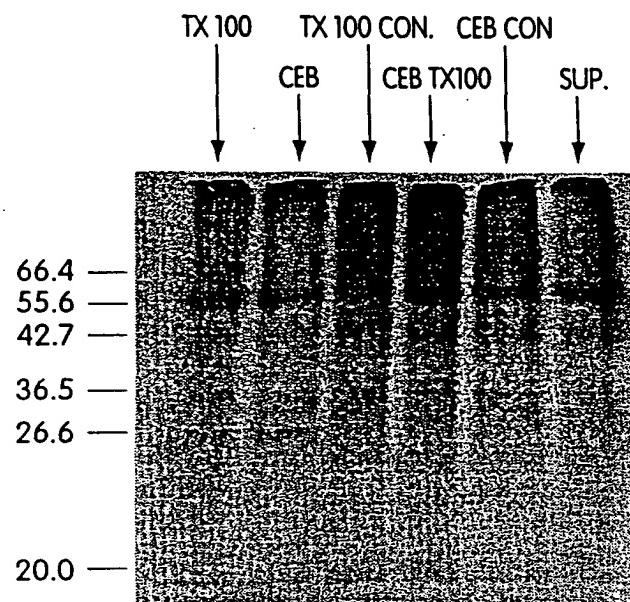


Fig. 23